

Identification of a Novel Maize Dehydration-Responsive Gene with a Potential Role in Improving Maize Drought Tolerance

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Abstract : Global climate change has resulted in altered rainfall patterns, which has resulted in annual losses in maize crop yields due to drought. Therefore it is important to produce maize cultivars that are more drought-tolerant, which is not an easily accomplished task as plants have a plethora of physical and biochemical adaptation methods. One such mechanism is the drought-induced expression of enzymatic and non-enzymatic proteins which assist plants to resist the effects of drought on their growth and development. One of these proteins is AtRD22 which has been identified in *Arabidopsis thaliana*. Using an in silico approach, a maize protein with 48% sequence homology to AtRD22 has been identified. This protein appears to be localized in the extracellular matrix, similarly to AtRD22. Promoter analysis of the encoding gene reveals cis-acting elements suggestive of induction of the gene's expression by abscisic acid (ABA). Semi-quantitative transcriptomic analysis of the putative maize RD22 has revealed an increase in transcript levels after the exposure to drought. Current work elucidates the effect of up-regulation and silencing of the maize RD22 gene on the tolerance of maize to drought. The potential role of the maize RD22 gene in maize drought tolerance can be used as a tool to improve food security.

Keywords : abscisic acid, drought-responsive cis-acting elements, maize drought tolerance, RD22

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